CLAIMS

What is claimed is:

1. An isolated nucleic acid molecule selected from the group consisting of SEQ ID NOS: 48-63 and 88-90.

2. An isolated nucleic acid molecule comprising a polynucleotide sequence at least 90% identical to a sequence selected from the group consisting of SEQ ID NOS: 48-56 and 88-90.

3. An isolated nucleic acid molecule comprising a polynucleotide sequence at least 90% identical to a sequence selected from the group consisting of SEQ ID NOS: 57-63.

4. An isolated nucleic acid molecule consisting of about 15 to 50 consecutive nucleotides from a nucleotide sequence according to Claim 2.

5. An isolated nucleic acid molecule consisting of about 20 to 50 consecutive nucleotides from a nucleotide sequence according to Claim 3.

6. An isolated nucleic acid molecule consisting of about 20 to 50 nucleotides which is the complement of a nucleic acid sequence according to Claim 4.

7. An isolated nucleic acid molecule consisting of about 20 to 50 nucleotides which is the complement of a nucleic acid according to Claim 5.

8. An isolated nucleic acid molecule comprising a polynucleotide sequence of about 20 to 50 nucleic acids which is at least 80% identical to a sequence according to Claim 2.

9. An isolated nucleic sequence molecule comprising a polynucleotide sequence of about 20 to 50 nucleic acids which is at least 80% identical to a sequence according to Claim 3.

10. An isolated nucleic sequence molecule selected from the group consisting of SEQ ID NOS: 30-47.

11. An isolated nucleic acid molecule which is the complement of a sequence according to Claim 10.

12. An isolated nucleic sequence molecule consisting of a polynucleotide sequence which is at least 90% identical to a sequence selected from the group consisting of SEQ ID NOS: 30-39.

13. An isolated nucleic sequence molecule consisting of at least a polynucleotide sequence which is at least 90% identical to a sequence selected from the group consisting of SEQ ID NOS: 40-47.

14. A method of detecting the presence or absence of a mutation or a polymorphism in a neuronal gene in a mammal, comprising the steps of:

(a) contacting a test sample comprising the neuronal gene with at least one nucleic acid sequence selected from the group consisting of SEQ ID NOS: 30-47;

(b) maintaining the test sample DNA and the nucleic acid sequence under conditions suitable for interaction; and

(c) detecting the interaction between the test sample DNA and the nucleic acid sequences.

15. The method of Claim 14, wherein the neuronal gene is selected from the group consisting of: TOR1A, TOR1B, TORP1, and TORP2.

16. The method of Claim 14, wherein the detecting step is performed by a nucleic acid amplification reaction.

17. The method of Claim 14, wherein the detecting step is performed by a single strand conformation polymorphism analysis.

18. The method of Claim 14, wherein the test sample is selected from the group consisting of a body fluid or a tissue sample.

19. The method of Claim 14, wherein the mammal is a human who is at increased risk of developing a neruonal disease selected from the group consisting of a movement disorder, a neurodegenerative disease, a neurodevelopmental disorder and a neuropsychiatric disease.

20. The method of Claim 14, wherein the mammal is a human afflicted with a neuronal disease selected from the group consisting of a movement disorder, a neurodegenerative disease, a neurodevelopmental disorder and a neuropsychiatric disease.

21. The method of Claim 14, wherein the neuronal gene is a gene located in the central nervous system or the peripheral nervous system.

22. The method of Claim 14, further comprising the steps of:

(d) isolating the test sample neuronal gene; and

(e) determining the sequence of the isolated gene.

23. The method of Claim 21, wherein the neuronal gene is located in the central nervous system in a region selected from the group consisting of cerebellum, locus ceruleus, substantia nigra and hippocampus.

24. A method of detecting the presence or absence of a dopamine-mediated disease in a mammal comprising detecting the presence or absence of one or more mutations in a neuronal gene, comprising the steps of:

(a) contacting a test sample comprising the neuronal gene with a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 30-47;

(b) maintaining the test sample and the nucleic acid sequence under conditions suitable for interaction; and

(c) detecting the interaction between the test sample and nucleic acid sequence.

25. The method of Claim 23, wherein the detecting step (c) is performed by a nucleic acid amplification reaction.

26. The method of Claim 23, where in the detecting step (c) is performed by single strand conformation polymorphism analysis.

27. A method of detecting the presence or absence of Parkinson's disease in a human comprising detecting the presence or absence of one or more mutations in a neuronal gene, comprising the steps of:

(a) contacting a test sample comprising the neuronal gene with a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 30-47;

(b) maintaining the test sample and the nucleic acid sequence under conditions suitable for interaction; and

(c) detecting the interaction between the test sample and nucleic acid sequence.

28. A gene comprising a gene mutation resulting in a dopamine-mediated disease in a mammal detected by a method comprising the steps of:

(a) contacting a test sample comprising the gene with a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 30-47;

(b) maintaining the test sample and the nucleic acid sequence under conditions suitable for interaction; and

(c) detecting the interaction between the test sample and nucleic acid sequence, wherein the gene mutation results in the dopamine-mediated disease.

29. A gene comprising a mutation or polymorphism responsible for a neuronal disease in a mammal detected by a method comprising the steps of:

(a) contacting a test sample comprising the gene with a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 30-47;

(b) maintaining the test sample and the nucleic acid sequence under conditions suitable for interaction; and

(c) detecting the interaction between the test sample and nucleic acid sequence, wherein the gene mutation results in the dopamine-mediated disease.

30. The method of Claim 29, wherein the neruonal disease is a disease selected from the group consisting of a movement disorder, a neurodegenerative disease, a neurodevelopmental disorder and a neurophyschiatric disease.